

Figure S3

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atHAC1      1  DTRHYFCIPCYNESRGDTILAEG-----TPMPKARLEKKNDEETEESWVQCDKCEAWQ
atHAC12    1  ETRHYFCIPCYNESRGDTILAEG-----TSMPKAKLEKKNDEEIEESWVQCDKCQAWQ
atHAC4     1  ESRHYVCAPCYNEAREKLVFLDG-----TSIPKTRLOKKNDEQVPEGWVQCDKCEAWQ
atHAC5     1  ESRHYVCIPCYNEARANTVSVDG-----TPVPKSRFEKKNDEEVEESWVQCDKCQAWQ
atHAC2     1  NAQHQICSPCHSRCKTKFPLCGV-----FIDKHKMLKRSNFDNADTEEWVQCESCEKWQ
hsCBP      1  QNRYHFCEKCFTEIQGENVTILGDDPSQPOTTISKDQFEKKNNDTLDPPEFVDCKECGRKM
mmCBP      1  QNRYHFCGKCFTEIQGENVTILGDDPSQPOTTISKDQFEKKNNDTLDPPEFVDCKECGRKM
hsp300     1  QNRYHFCEKCFNEIQGESVSLGDDPSQPOTTINKEQFSKRKNNDTLDPPELFVECTECGRKM
dmCBP      1  SNRYTYCQKCFNDIQGDTVTLGDDPLQSQQTQIKKQDFKEMKNDHLELEPFVNCQECGRKQ
ceCBP-1    1  TERYTYCQKCFDALPPEGISLSENPNDRNNMAPKTSFTEQKNSVIDYEPFERCKYCMRWK
  
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atHAC1      55  HQICALFNGRRNDGGQAEYTCPYCFIAEVEQSKRKL PQSAVLGAKDLPRITILSDHIEQR
atHAC12    55  HQICALFNGRRNDGGQAEYTCPYCVIDVEQNERKPL LQSAVLGAKDLPRITILSDHIEQR
atHAC4     55  HTICALFNSRRNHGESTKYTCPSCYIQEVEQRERRPL PLSAVPGATSLPVTLSLKHLEER
atHAC5     55  HQICALFNGRRNHGQ-AEYTCPNICYIQEVEQGERKPV SQNVILGAKSLPASTLSNHLEQR
atHAC2     55  HQICGLYNKDKDEDKTAEYICPTCLLEECQSINMAL VDYTDSGAKDLPETVLSYFLEQR
hsCBP      61  HQICVLHYDIIWPSG---FVCDNCLKKTGRPRKEN-----KFSAKRLQTTTLGNHLEDR
mmCBP      61  HQICVLHYDIIWPSG---FVCDNCLKKTGRPRKEN-----KFSAKRLQTTTLGNHLEDR
hsp300     61  HQICVLHHEIIPAG---FVCDGCLKKSARTRKEN-----KFSAKRLPSTRILGTFLLENR
dmCBP      61  HQICVLWLDIIPGG---FVCDNCLKKKNKSKRKEN-----KFNAKRLPTTKLGVYIETR
ceCBP-1    61  HRIICALHDKKVPPEG---FICECRTAKKYQKPDN-----KYLASKLPHNKLSTFLEDR
  
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atHAC1      115 LFKRLKQERTERARAQGSYDEIPTAESLVIRVVS SVDKKLEVKPRFLEIFREDS-YPTE
atHAC12    115 LFKRLKQERTERARVQGTSYDEIPTVESLVVRVVS SVDKKLEVKSRLFLEIFREDN-FPTE
atHAC4     115 LFKKLKEERQERARLQKTYEEVPGAESLTVRVVAS VDKVLEVKERFLELFREEEN-YPSE
atHAC5     114 LFKKLKQERQERARLQKSYEEVPGADSLVIRVVAS VDKILEVKPRFLDIFREDN-YSSE
atHAC2     115 LFKRLKEERYQTAKATGKSINDVPEPEGLTLRVVFS ADRTLITVINKQFASLLHKEN-FPSE
hsCBP      112 VNKFLRRONHPEAG-----EVFVRVVASDKTVEVKP GMKSRFVDSGEMSES
mmCBP      112 VNKFLRRONHPEAG-----EVFVRVVASDKTVEVKP GMKSRFVDSGEMSES
hsp300     112 VNDFLRRONHPEAG-----EVTVRVHASDKTVEVKP GMKARFVDSGEMAES
dmCBP      112 VNNFLKKKEAG-AG-----EVHIRVVS SDKCVKVEVKPMRRRFVEQGEMMNE
ceCBP-1    112 VNGFIKKQLQAEAHK---Y-----PVIIRTL CVQDKEAEVKAQMKQKYVESNQFPEK
  
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atHAC1      174 FAYKSKVLLLFQKIEGVEVCLFGMYVQEFQSECAF PNQRRVYLSYLDVSKYFRPEVRSYN
atHAC12    174 FPKSKVLLLFQKIEGVEVCLFGMYVQEFQSECSNP NQRRVYLSYLDVSKYFRPDIKSAN
atHAC4     174 FPKSKAIFLFQKIENVEVCLFGMFVQEFQSDSGP PNERR-----FR--TVS--
atHAC5     173 FPKSKAIFLLFQKIEGVEVCLFGMYVQEFQSDSAS PNQRRVYLSYLDVSKYFRPDVRTVS
atHAC2     174 FPKSKVLLLFQKVHGVDCIFALFVQEFQSECSQP NQRSTYIFYLDSVKYFKPERVTFA
hsCBP      159 FPKRKALFAFEEIDGVVDCFFGMHVQEYGSDCPP PNTRRVYISYLDVSHFFRPR-----
mmCBP      159 FPKRKALFAFEEIDGVVDCFFGMHVQEYGSDCPP PNQRRVYISYLDVSHFFRPR-----
hsp300     159 FPKRKALFAFEEIDGVVDCFFGMHVQEYGSDCPP PNQRRVYISYLDVSHFFRPR-----
dmCBP      158 FPKRKALFAFEEIDGVVDCFFGMHVQEYGSCEPAP NTRRVYIAYLDSVHFFRPR-----
ceCBP-1    161 FPKRKALFAFEEIDGVEVCFGLHVQEYGSACPA PNARRVYIAYLDSVHFFQPR-----
  
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atHAC1      234 GEALRTFVYHEILIGYLEYCKLRGFTSCYIWACPPL KGEDYILYCHPEIQKTPKSDKLR
atHAC12    234 GEALRTFVYHEILIGYLEYCKLRGFTSCYIWACPPL KGEDYILYCHPEIQKTPKSDKLR
atHAC4     220 GEALRTFVYHEILIGYLDYCKKRGFTSCYIWACPPL KGDDYILYCHPEIQKTPKTDKLR
atHAC5     233 GEALRTFVYHEILIGYLDYCKKRGFSSCYIWACPPL KGEDYILYCHPEIQKTPKTDKLR
atHAC2     234 GEALRTFVYHEVILIGYLEYCKLRGFTTSYIWACPP KI GQDYIMYSHPKTQQTPTDKLRK
hsCBP      214 --CLRTAVYHEILIGYLEYVKKLGYVTGHIWACPP SEGDDYIFHCHPPDQKIPKPKRLQE
mmCBP      214 --CLRTAVYHEILIGYLEYVKKLVYVTAHIWACPP SEGDDYIFHCHPPDQKIPKPKRLQE
hsp300     214 --CLRTAVYHEILIGYLEYVKKLGYVTGHIWACPP SEGDDYIFHCHPPDQKIPKPKRLQE
dmCBP      213 --QYRTAVYHEILIGYMDYVKKQLGYTMAHIWACPP SEGDDYIFHCHPTDQKIPKPKRLQE
ceCBP-1    216 --ELRTDVYHEILLGYLDYAKMLGYTMAHIWACPP SEGDDYIFHCHPPEQKIPKPKRLQD
  
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atHAC1      294 WYLAMLRKASKEGIVAETINLYDHFFMQTGECRAKV TAARLPYFDGDYWPAAEDLIYQM
atHAC12    294 WYLAMLRKAAKEGIVAETTNLYDHFFLQTGECRAKV TAARLPYFDGDYWPAAEDIISQM
atHAC4     280 WYLAMLRKASKEDVVVECTNLYNHFFVQSGECRANV TAARLPYFDGDYWPAAEDLLRQM
  
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atHAC5 293 WYLAMLLKASKEKVVVECTNFYDHFVQSGEGRKAVTAARLPYFDGDYWPAAEDLIDQM
atHAC2 294 WYVSMLOKAAEQRVVMNVTNLYDRFFDST---EELYMTAARLPYFEFSGFWSNRAEIMIQDI
hsCBP 272 WYKMLDKAFAERI IHDYKDI FKQATEDR-----LTSAKELPYFEGDFWPNVLEESIKEL
mmCBP 272 WYKMLDKAFAERI IHDYKDI FKQANEDR-----LTSAKELPYFEGDFWPNVLEESIKEL
hsp300 272 WYKMLDKAVSERIVHDYKDI FKQATEDR-----LTSAKELPYFEGDFWPNVLEESIKEL
dmCBP 271 WYKMLDKGMIERI IQDYKDI LKQAMEDK-----LGSAAELPYFEGDFWPNVLEESIKEL
ceCBP-1 274 WYKMLEKGVQEGSVVEFKDIYKQARDN-----LTTPTQLPYFEGDFWPNVIEDCIREA

atHAC1 354 SQEEDGRKGNKKGMLKKTITKRALKASGQTDLSGNASKDLLLMHRLGETIHPMKEDFIMV
atHAC12 354 SQEDDGRKGNKKGILKKPITKRALKASGQSDFSGNASKDLLLMHKLGETIHPMKEDFIMV
atHAC4 340 NQEDGETKLHRKGLTKKVISKRALKAVGQLDLSLNASKDRLMMQKLGETICPMKEDFIMV
atHAC5 353 SQEEDGKKSNRKLMPKKVISKRALKAVGQLDLSVNASKDLLLMHKLGEIILPMKEDFIMV
atHAC2 351 EREGNNELOKQKVKLSRRKVKTMSYKTTG-DVDVDDVKNILLMEKLEKEVFPNKKDLMVV
hsCBP 327 EQEEERKKEESTAASETTEGSQGDSKNAKKKNNKKTINKNKSSIS-----
mmCBP 327 EQEEERKKEESTAASETPEGSQGDSKNAKKKNNKKTINKNKSSIS-----
hsp300 327 EQEEERKREENTSN-ESTDVTKGDSKNAKKKNNKKTINKNKSSLS-----
dmCBP 326 DQEEERKQAEAAEAAAAANLFSIEENEVSGDGKKKGQKKAKKSNKSKAA-----
ceCBP-1 329 SNEEAQRKVKEDDDGDADGGLGGGDSGKKKSSKNNKNNLKKNA-----

atHAC1 414 HLOPSCTHCCILMVSNGNRWVCSQCKHFQICDKCYEAEQRREDRERHPVNFKDKHALY-PV
atHAC12 414 HLOHSCTHCCTLMVTCNRWVCSQCKDFQLCDGCEAEQKREDRERHPVNQDKHNIF-PV
atHAC4 400 HLOHCCKHCTTLMVSGNRWVCHCKNFQICDKCYEVEQNRINIERHPINQKEKHALF-PV
atHAC5 413 HLOHCCKHCTTLMVSGNRWVCHCKNFQICDKCHEVEENRVEKEKHPVNQKEKHALY-PV
atHAC2 410 ELNYSCTRC SKAVLSGLRWFCEKCKNLHLCESCYDAGQELPGEHIYKRM DKEKHQLSKVQ
hsCBP 372 -----RANKKKPSMPNVSNDLSQKLYATMEKHKEVFFVIHLHAGPV
mmCBP 372 -----RANKKKPSMPNVSNDLSQKLYATMEKHKEVFFVIHLHAGPV
hsp300 371 -----RGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRL IAGPA
dmCBP 377 ---Q-----RKNSKKSNEHQSGNDLSTKIYATMEKHKEVFFVIRLHSAQS
ceCBP-1 374 -----KMNKKKAGSITGNEVADKLYSQFEKHKEVFFTIRLVSLQN

atHAC1 473 EIMDI PADTRKDEILESEFFDTRQAFSLCQGNHYQYDTLRRAKHSSMMVLYHLHNP
atHAC12 473 EIADI PTDTKDRDEILESEFFDTRQAFSLCQGNHYQYDTLRRAKHSSMMVLYHLHNP
atHAC4 459 AIKDVPTKIEDKNNLESEFFHNROAFNL CQGNHYQYETLRRAKHSSMMILYHLHNP
atHAC5 472 AIDNIPTEIKDNDILESEFFDTRQAFSLCQGNHYQYDTLRRAKHSSMMILYHLHNP
atHAC2 470 VNGVLFSTTEDNDI IQENDMFESRQAF LAFS QKHNYNFHTLRHAKHSSMMILHHLHTS
hsCBP 413 INTL- PPI -VDPDPLLSCDLMDGRDAFLTLARDKHWEFSSLRRSKWSTLCMLVELHTQ
mmCBP 413 ISTQ- PPI -VDPDPLIPC DLMGRDAFLTLARDKHLEFSSLRRAQWSTLCMLVELHTQ
hsp300 412 ANSL- PPI -VDPDPLIPC DLMGRDAFLTLARDKHLEFSSLRRAQWSTLCMLVELHTQ
dmCBP 419 AASL- API -QDPDPLITCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTLCMLVELHTQ
ceCBP-1 414 EPAVLAKPISDPDGLMQSDMMMDGRDTFLT KAREEHWEFSSLRRAKYSTLCIAYSLHET

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Figure S3

Multiple sequence alignment of the acetyltransferase domains of the CBP type proteins. The numbers listed in front of the sequences indicates the location in the domain and not in the given protein sequence.